

WHAT IS CLAIMED IS:

Claim 1. A system for determining the level of a biological indicator within a patient sample applied to an arrayed information structure, where the arrayed information structure emits data indicative of the biological indicator, based on digitized output patterns from the arrayed information structure, comprising:

a preconditioning unit for pre-conditioning the digitized output pattern;

an interferometric unit configured to generate an interference between the pre-conditioned digitized output pattern and a reference wave to enhance the digitized output pattern; and

an analysis unit for analyzing the interferometrically enhanced digitized output pattern to determine the level of the biological indicator.

Claim 2. A system for determining the level of specific constituents within an output pattern generated from a detected image of a biological sample applied to an array wherein the output pattern comprises signals associated with noise, and signals associated with the biological sample which have intensities both greater and less than intensities of signals associated with noise, comprising:

tessellation means for tessellating the output pattern;

signal processing means for amplifying signals associated with the biological sample within the tessellated output pattern, having an intensity lower than the intensity of signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

first determination means for determining which signals within the modified output pattern correlate with specific constituents within the biological sample;

second determination means for determining specific constituents within the biological sample based on the signals within the modified output pattern correlating to specific constituents within the biological sample; and

third determination means for associating the signals correlating to specific constituents with levels of such specific constituents within the sample.

Claim 3. A system for quantitating specific constituents within an output pattern generated from a detected image of a biological sample applied to an array wherein the output pattern comprises signals associated with noise, and signals associated with the biological sample which have intensities both greater and less than intensities of signals associated with noise, comprising:

a tessellation unit for segmenting the output pattern;

a signal processing unit to amplify signals associated with the biological sample within the segmented output pattern, having an intensity lower than the intensity of signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

a first determination unit to determine which signals within the modified output pattern correlate with specific constituents within the biological sample;

a second determination unit to determine specific constituents within the biological sample based on the signals within the modified output pattern correlating to specific constituents within the biological sample; and

a mapping unit for mapping the signals correlating to specific constituents on a diffusion curve to determine the level of such specific constituents within the biological sample.

Claim 4. A technique for analyzing an output pattern of a biological sample applied to an array to determine the presence and quantity of specific constituents within a biological sample applied to the array, wherein the output pattern comprises signals associated with noise, and signals correlating to the biological sample with the signals correlating to the biological sample having intensities both greater and less than the signals associated with noise, the method comprising the steps of:

segmenting the output pattern of the array using tessellation;

interferometrically enhancing the segmented output pattern to amplify signals associated with the biological sample, having an intensity lower than the intensity of signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

associating signals within the interferometrically enhanced segmented output pattern with specific constituents within the biological sample; and

determining specific constituents within the biological sample based on the signals within the interferometrically enhanced segmented output pattern associated with specific constituents within the biological sample; and

mapping the signals associated with specific constituents to a diffusion curve.

Claim 5. A computer code product that determines the presence of specific constituents within an output pattern of a biological sample applied to an array of detectors, wherein the output pattern comprises signals associated with noise, and signals associated with the biological sample which have intensities both greater and less than intensities of signals associated with noise, the computer code product comprising:

computer code that segments the output pattern using tessellation;

computer code that utilizes signal processing to amplify signals within the segmented output pattern associated with the biological sample having an intensity lower than the intensity of the signals associated with noise, to an intensity greater than the intensity of the signals associated with noise to generate a modified output pattern;

computer code that determines which signals within the modified output pattern correlate with specific constituents within the biological sample; and

computer code that determines specific constituents within the biological sample based on the signals within the modified output pattern correlating to specific constituents within the biological sample; and

computer code that maps signals correlating to specific constituents to a diffusion curve.

Claim 6. A method for determining the effectiveness of a therapy by analyzing microarray output patterns generated from two or more biological samples taken from a patient undergoing the therapy comprising the steps of:

generating a diffusion curve with a therapy of interest;

mapping the output patterns to the diffusion curve;

determining the degree of convergence between the mapped coordinates of the respective output patterns mapped on the diffusion curve.

Claim 7. The method of claim 6 further comprising the step of interferometrically enhancing the output patterns prior to the mapping step.

Claim 8. The method of claim 7 wherein the interferometric enhancement step
5 utilizes resonance interferometry.

Claim 9. The method of claim 8 wherein the resonance interferometry is either quantum resonance interferometry or stochastic resonance interferometry.

10 Claim 10. The method of claim 7 further comprising the step of tessellating the output pattern prior to the interferometric enhancement step.

Claim 11. The method of claim 6 further comprising the step of performing nucleic acid amplification to enhance the output patterns prior to the mapping step.

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Claim 12. The method of claim 6 wherein the sample is selected from a group consisting of DNA, RNA, protein, peptide-nucleic acid (PNA) and targeted nucleic acid (TNA) samples.